

Fig. 1 (continued)

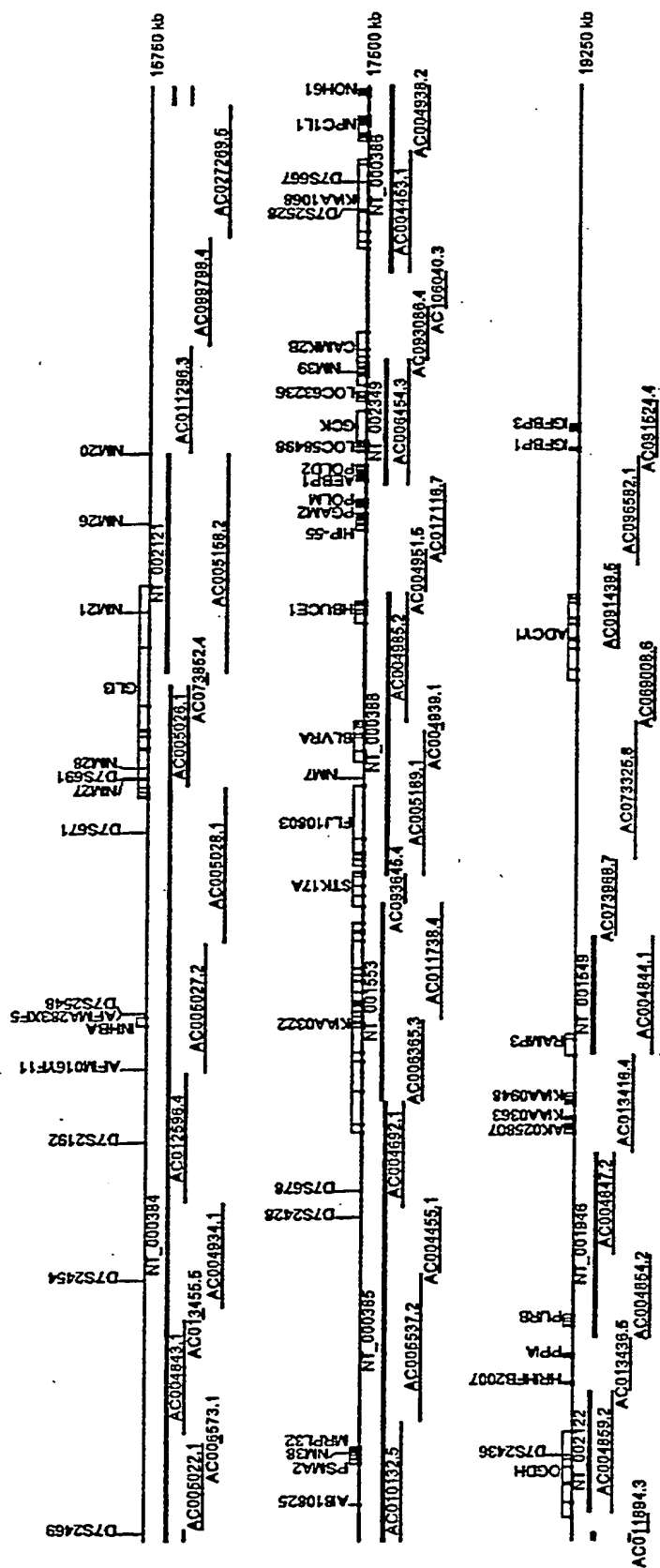


Fig. 1 (continued)

10/539565

4/42

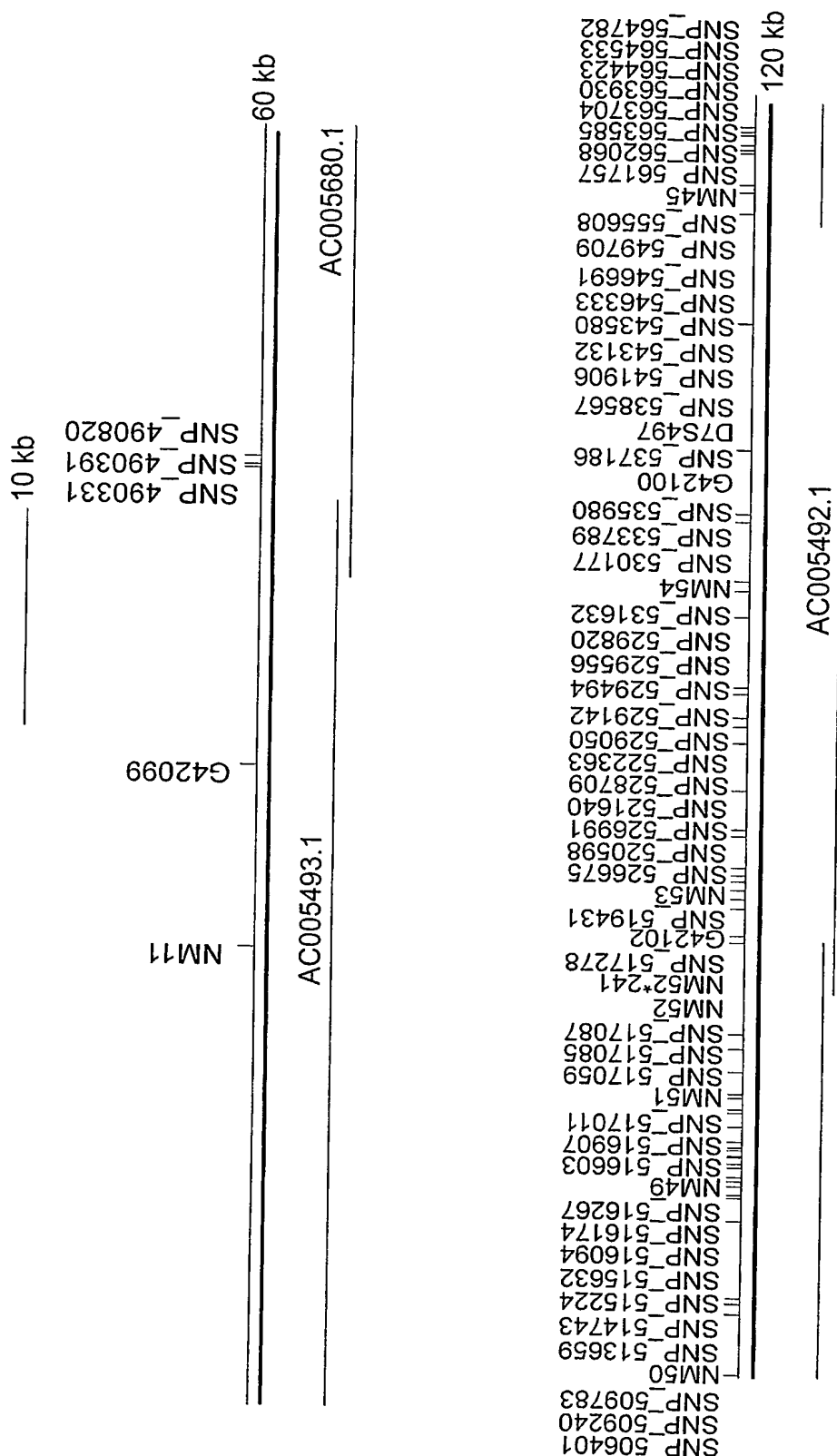


Fig. 2

10/539565

5/42

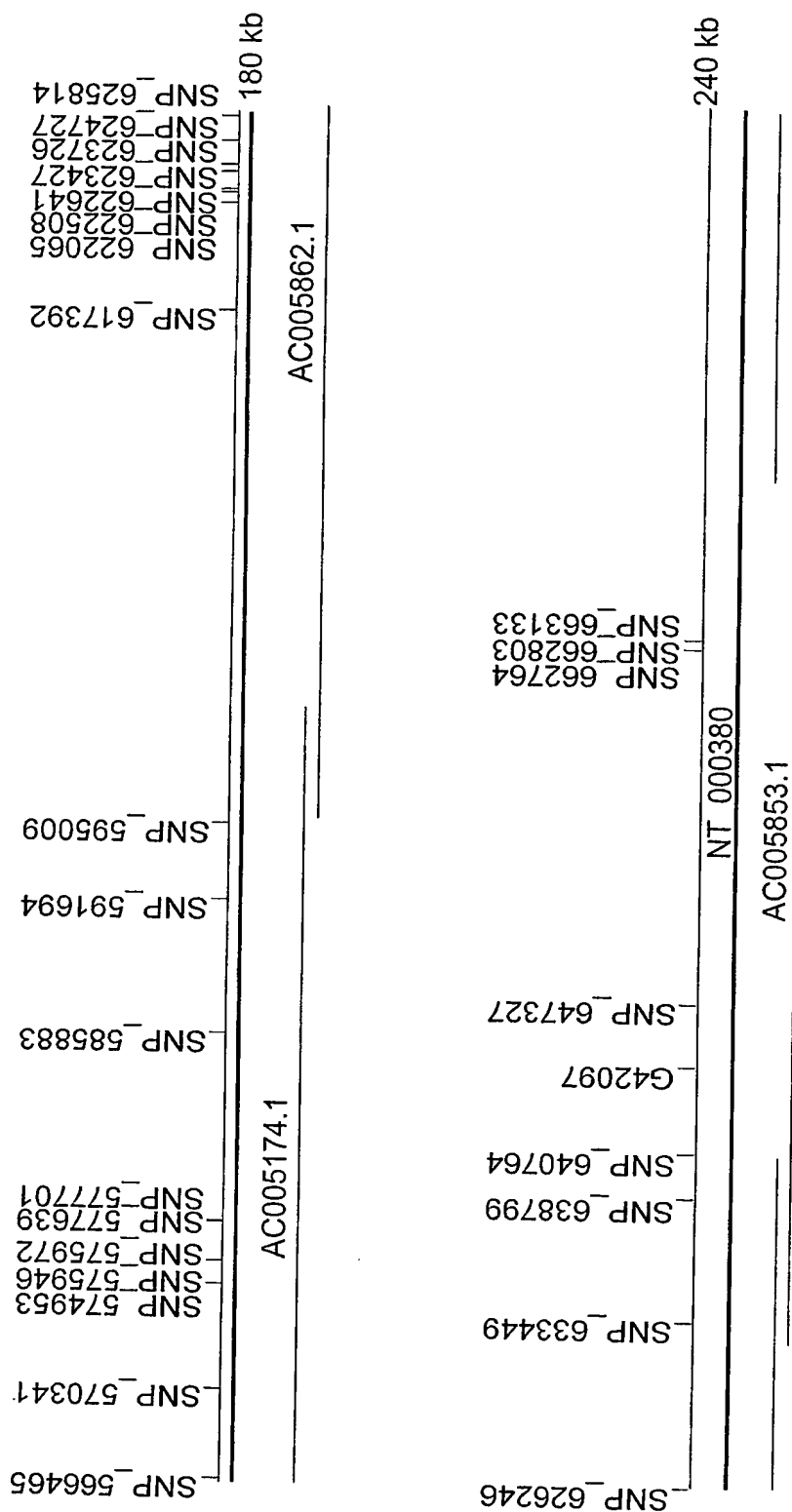
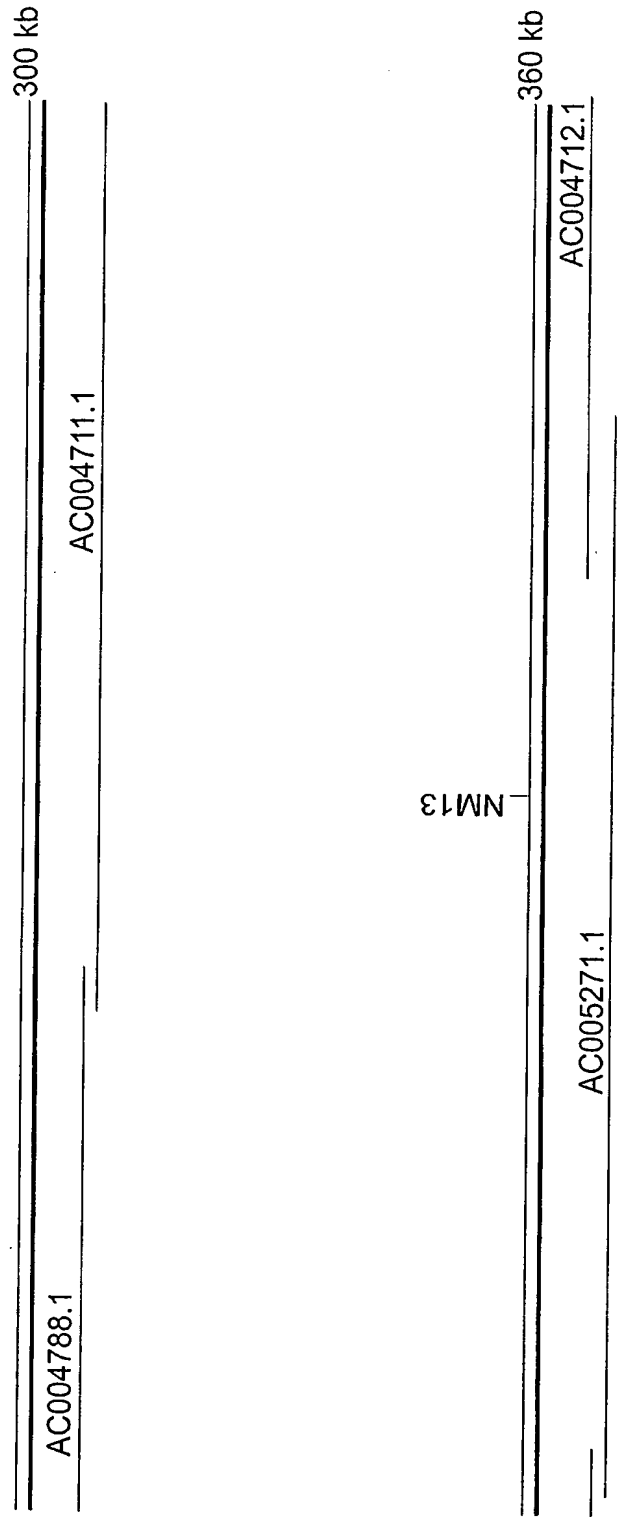


Fig. 2 (Continued)



NM13

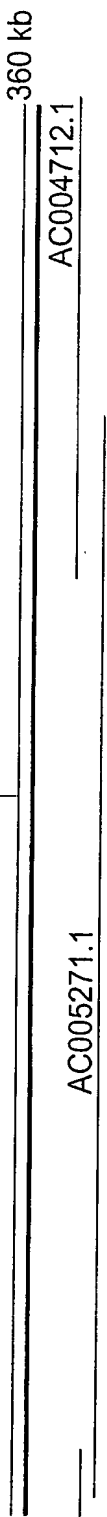


Fig. 2 (Continued)

10/539565

7/42

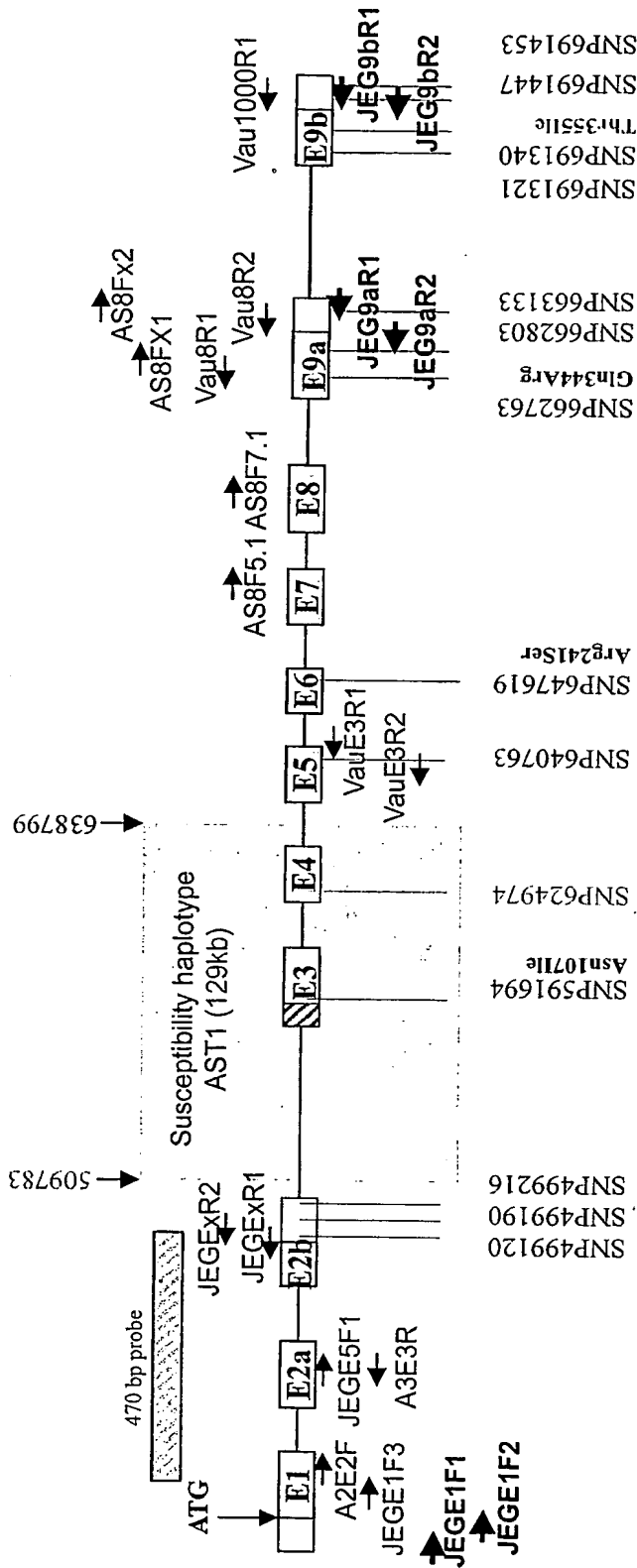


Fig. 3

Figure 4A**A SEQ ID NOs: 2 and 3 (GB AY310326)**

ggagggctctgtgcctccgttcagcagagctgcagctgctgccagctctcaggaggcaa
gctggactccctcactcagctgcaggagcaaggacagtgaggctcaaccccgctgagcc
atgccagccaacttcacagagggcagcttcgattccagtgaggaccgggcagacgctggat
M P A N F T E G S F D S S G T G Q T L D
tcttccccagtggttgactgaaacagtgacttttactgaagtggaggaaaggaa
S S P V A C T E T V T F T E V V E G K E
tggggttccttctactactcctttaag|actgagcaattgataactctgtgggtcctcttt
W G S F Y Y S F K T E Q L I T L W V L F
gtttttaccattgttgaaactccgttgtgctttttccacatggaggagaaagaagaag
V F T I V G N S V V L F S T W R R K K K
tcaagaatgaccttcttctgtgactcagctggccatcacag|attcctttcacaggactggtc
S R M T F F V T Q L A I T D S F T G L V
aacatcttgacagatattaattggcgattcactggagacttcacggcacctgacctgggt
N I L T D I N W R F T G D F T A P D L V
tgccgagtggtccgctatttgcag|gttgtgctgctctacgctctacctacgtcctgggtg
C R V V R Y L Q V V L L Y A S T Y V L V
tccctcagcatagacagataccatgccatcgtctaccccatgaagttccttcaaggag|aa
S L S I D R Y H A I V Y P M K F L Q G E
aagcaagccagggtcctcattgtgatcgctggagcctgtcttttctgttctccattccc
K Q A R V I V I A W S L S F L F S I P
accctgatcatatttgggaagaggacactgtccaacgggtgaagtgcagtgctggccctg
T L I I F G K R T L S N G E V Q C W A L
tggcctgacgactcctactggaccccatatgacctcgtggccttctggtgtacttc
W P D D S Y W T P Y M T I V A F L V Y F
atccctctgacaatcatcag|catcatgtatggcattgtgatccgaactatttggattaaa
I P L T I I S I M Y G I V I R T I W I K
agcaaacctacgaaacagtgatttccaactgctcag|atgggaaactgtgcagcagctat
S K T Y E T V I S N C S D G K L C S S Y
aaccgaggactcatctcaaaggcaaaaatcaaggctatcaagtatagcatcatcatt
N R G L I S K A K I K A I K Y S I I I I
cttg|ccttcatctgctgttggagtccatacttctgtttgacattttggacaatttcaac
L A F I C C W S P Y F L F D I L D N F N
ctccttccagacacccaggagcgtttctatgcctctgtgatcattcagaacctgccagca
L L P D T Q E R F Y A S V I I Q N L P A
ttgaatagtgccatcaacccccctcatctactgtgtcttcagcagctccatctcttcccc
L N S A I N P L I Y C V F S S S I S F P
tgcag|ggagcaaagatcacaggattccagaatgacgttccgggagagaactgagaggcat
C R E Q R S Q D S R M T F R E R T E R H
gagatgcagattctgtccaagccagaattcatctagaccctagggcagtgccagtgctag
E M Q I L S K P E F I *
gctgagcaccatcagctctcccagggtccttgtcacctgcttgggcacgtgcatggaaccc
gagccaacttcacccacccctcgtcattacctgggagatgcacaagacaaatgttcta
gactgcatgcactgcttaagtattggccaacacgaactccccagttattcatgccagcca
ggaaggaaacgccttcttccccaccattcccagccctccttcccactggccagcacctg
aaccagtgaaacagagcattagtgggtccagggtcctggcttgagaccagtgagtagac

10/539563

9/42

Figure 4B1**B long SEQ ID NOS: 4 and 5 (GB AY310327)**

ggggtcag
ggagggctctgtgcctccgttcagcagagctgcagctgctgccagctctcaggaggcaa
gctggactccctcactcagctgcaggagcaaggacagtgaggctcaacccgcctgagcc
atgccagccaacttcacagagggcagcttcgattccagtgaggaccgggcagacgctggat
M P A N F T E G S F D S S G T G Q T L D
tcttcccagtggttgactgaaacagtgacttttactgaagtggaggaaaggaa
S S P V A C T E T V T F T E V V E G K E
tggggttccttctactactcctttaag|actgagcaattgataactctgtgggtcctcttt
W G S F Y Y S F K T E Q L I T L W V L F
gtttttaccattgttgaaactccgttgctgtttttccacatggaggagaaagaagaag
V F T I V G N S V V L F S T W R R K K K
tcaagaatgaccttctttgtgactcagctggccatcacag|attctttcacaggactggc
S R M T F F V T Q L A I T D S F T G L V
aacatcttgacagatattaattggcgattcactggagacttcacggcacctgacctgggt
N I L T D I N W R F T G D F T A P D L V
tgccgagtggtccgctatttgag|gttggtgctgctctacgcctctacctacgtcctgggtg
C R V V R Y L Q V V L L Y A S T Y V L V
tccctcagcatagacagataccatgccatcgtctaccccatgaagttccttcaaggag|aa
S L S I D R Y H A I V Y P M K F L Q G E
aagcaagccagggctcctcattgtgatcgccctggagcctgtcttttctgttctccattccc
K Q A R V L I V I A W S L S F L F S I P
accctgatcatatttggaagaggacactgtccaacgggtgaagtgcagtgctggccctg
T L I I F G K R T L S N G E V Q C W A L
tggcctgacgactcctactggaccccatatgaccatcgtggccttctggtgtacttc
W P D D S Y W T P Y M T I V A F L V Y F
atccctctgacaatcatcag|catcatgtatggcattgtgatccgaactatttgattaaa
I P L T I I S I M Y G I V I R T I W I K
agcaaaccttacgaaacagtgatttccaactgctcag|atgggaaactgtgcagcagctat
S K T Y E T V I S N C S D G K L C S S Y
aaccgaggactcatctcaaaggcaaaaatcaaggctatcaagtatagcatcatcatt
N R G L I S K A K I K A I K Y S I I I I
cttg|ccttcatctgctgttgaggatccatacttctgtttgacattttggacaatttcaac
L A F I C C W S P Y F L F D I L D N F N
ctccttccagacacccaggagcgtttctatgcctctgtgatcattcagaacctgccagca
L L P D T Q E R F Y A S V I I Q N L P A
ttgaatagtgccatcaacccctcatctactgtgtcttcagcagctccatctctttcccc
L N S A I N P L I Y C V F S S S I S F P
tgcag|ggctatccgtctccgtcagctccaggaggtgcgctaagtctctgccctcaacga
C R V I R L R Q L Q E A A L M L C P Q R
gagaactggaagggtacttggccaggtgtaccttctgggtcttccaagggtgacagctc
E N W K G T W P G V P S W A L P R *
tcacctgtgctgcaggtggccctgtgcctgggtgccacttctcactgcttaccagggcac
aaggacaccagtggttcccaaatgggtcacagcaggatggcctgcatcagattcaccag
ggagggctataagaaggcagac

Figure 4B2**B short SEQ ID NOS: 6 and 7 (GB AY310328)**

ggggtcag
ggagggctctgtgcctccgttcagcagagctgcagctgctgccagctctcaggaggcaa
gctggactccctcactcagctgcaggagcaaggacagtgaggctcaaccccgccctgagcc
atgccagccaacttcacagagggcagcttcgattccagtgaggaccgggcagacgctggat
M P A N F T E G S F D S S G T G Q T L D
tcttccccagtggttgcactgaaacagtgacttttactgaagtgggtggaaggaaaggaa
S S P V A C T E T V T F T E V V E G K E
tgggggttccttctactactcctttaag|actgagcaattgataactctgtgggtcctcttt
W G S F Y Y S F K T E Q L I T L W V L F
gtttttaccattgttggaaactccgttgtgctttttccacatggaggagaaagaagaag
V F T I V G N S V V L F S T W R R K K K
tcaagaatgaccttcttctgtgactcagctggccatcacag|atattaattggcgattcact
S R M T F V T Q L A I T D I N W R F T
ggagacttcacggcacctgacctgggttgcagtggtccgctattttgcag|gttgtgctg
G D F T A P D L V C R V V R Y L Q V V L
ctctacgcctctacctacgtcctggtgtccctcagcatagacagataccatgccatcgctc
L Y A S T Y V L V S L S I D R Y H A I V
taccatgaagttccttcaaggag|aaaagcaagccagggtcctcattgtgatcgccctgg
Y P M K F L Q G E K Q A R V L I V I A W
agcctgtcttttctgttctccattccaccctgatcatatttgggaaggagacactgtcc
S L S F L F S I P T L I I F G K R T L S
aacgggtgaagtgcagtgctgggcccctgtggcctgacgactcctactggaccccatacatg
N G E V Q C W A L W P D D S Y W T P Y M
accatcggtggccttctggtgtacttcatccctctgacaatcatcag|catcatgtatggc
T I V A F L V Y F I P L T I I S I M Y G
attgtgatccgaactatttggattaaaagcaaaacctacgaaacagtgatttccaactgc
I V I R T I W I K S K T Y E T V I S N C
tcag|atgggaaactgtgcagcagctataaccgaggactcatctcaaaggcaaaaatcaag
S D G K L C S S Y N R G L I S K A K I K
gctatcaagtatagcatcatcatcattcttg|ccttcatctgctgttggagtccatacttc
A I K Y S I I I I L A F I C C W S P Y F
ctgtttgacatttttgacaatttcaacctccttccagacacccaggagcgtttctatgcc
L F D I L D N F N L L P D T Q E R F Y A
tctgtgatcattcagaacctgccagcattgaatagtgccatcaacccccctcatctactgt
S V I I Q N L P A L N S A I N P L I Y C
gtcttcagcagctccatctcttccccctgcag|ggatcatccgtctccgtcagctccaggag
V F S S S I S F P C R V I R L R Q L Q E
gctgcgctaattgctctgccctcaacgagagaactggaaggggtacttggccagggtgtacct
A A L M L C P Q R E N W K G T W P G V P
tcctggggtcttccaaggtgacagctctcaccctgtgctgcaggtggccctgtgcctggt
S W A L P R *
gccacttctcactgcttaccagggcacaaggacaccagtgggttcccaaaatgggtcacag
caggatggcctgcatcagattcaccagggagggtataagaaggcagac

10/539565

11/42

Figure 4C

C SEQ ID NOS: 8 and 9 (GB AY310329)

```
ggagggctctgtgcctccgttcagcagagctgcagctgctgcccagctctcaggaggcaa
gctggactccctcaactcagctgcaggagcaaggacagtgaggctcaacccgcctgagcc
atgccagccaacttcacagagggcagcttcgattccagtgggaccgggcagacgctggat
M P A N F T E G S F D S S G T G Q T L D
tcttccccagtggttgactgaaacagtgacttttactgaagtggggaaggaaaggaa
S S P V A C T E T V T F T E V V E G K E
tggtgttccttctactactcctttaag|actgagcaattgataactctgtgggtcctcttt
W G S F Y Y S F K T E Q L I T L W V L F
gtttttaccattgttgaaaactccgttgcttttttccacatggaggagaaagaagaag
V F T I V G N S V V L F S T W R R K K K
tcaagaatgaccttctttgtgactcagctggccatcacag|tataacaagcccacctgctt
S R M T F F V T Q L A I T V *
gagctgggctgcagtgccagggtaaacatccaaggcaccagtgaataacacagagaagg
taaaaggagcaagagttctgaagatggaacctgggatgggggaaagtcttctcaatcttt
cctaccaacaagaactccaatttttcactcctataaccgtagaagtagaggttaattagga
tcatccagcaaatgcttagaggcaaatatccctggatgaggatgccacagcttattttca
ttatatttcttcgattacagtgttggaatgcatgttgatggaactacatattctttcag
aatgaaaggatttagaggtggcaagaatatcagcttgaaatttaaagttttttcataaac
aataaacaatgataattgaaaattc
```

Figure 4D

D SEQ ID NOS: 10 and 11 (GB AY310330)

gggctcag
ggagggctctgtgcctccgttcagcagagctgcagctgctgccagctctcaggaggcaa
gctggactccctcactcagctgcaggagcaaggacagtgaggctcaaccccgctgagcc
atgccagccaacttcacagagggcagcttcgattccagtgggaccgggcagacgctggat
M P A N F T E G S F D S S G T G Q T L D
tcttccccagtggttgactgaaacagtgacttttactgaagtgggtggaaggaaaggaa
S S P V A C T E T V T F T E V V E G K E
tggggttccttctactactcctttaag|actgagcaattgataactctgtgggtcctcttt
W G S F Y Y S F K T E Q L I T L W V L F
gtttttaccattgttggaactccgttgctgtttttccacatggaggagaagaagaag
V F T I V G N S V V L F S T W R R K K K
tcaagaatgaccttctttgtgactcagctggccatcacag|gttggtgctgctctacgcctc
S R M T F F V T Q L A I T G C A A L R L
tacctacgtcctgggtgctccctcagcatagacagataccatgccatcgtctaccccatgaa
Y L R P G V P Q H R Q I P C H R L P H E
gttccttcaaggag|aaaagcaagccagggctcctcattgtgatcgctggagcctgtcttt
V P S R R K A S Q G P H C D R L E P V F
tctgttctccattcccaccctgatcatatttggaagaggacactgtccaacgggtgaagt
S V L H S H P D H I W E E D T V Q R *
gcagtgtggggccctgtggcctgacgactcctactggaccccatatgaccatcgtggc
cttcctgggtgtacttcatccctctgacaatcatcagcatcatgtatggcattgtgatccg
aactatttggattaaaagcaaacctacgaaacagtgatttccaactgctcagatgggaa
actgtgcagcagctataaccgaggactcatctcaaaggcaaaaatcaaggctatcaagta
tagcatcatcatcattcttgcccttcatctgctgttgaggatccataacttctgtttgacat
tttggaacaatttcaacctccttccagacacccaggagcgtttctatgcctctgtgatcat
tcagaacctgccagcattgaatagtgccatcaacccctcatctactgtgtcttcagcag
ctccatctctttcccctgcaggagcaaatgacagattccagaatgacgttccggga
gagaactgagaggcatgagatgcagattctgtccaagccagaattcatctagaccctagg
gcagtgccagtgttaggctgagcaccatcagctctcccaggctcctgtcacctgcttggg
cacgtgcatggaacccgagccaacttcacccaccctcgtcattacctgggagatgcaca
agacaaatgttctaagtactgcatgcactgcttaagtattggccaacacgaactccccag
ttattcatgccagccaggaaggaaacgccttccctccccaccattcccagccctcctcc
cactggccagcacctgaacccagtgaacacaggcattagtgggtccagggtcctggcttgg
agccagtgagtagac

10/539565

13/42

Figure 4E**E SEQ ID NOS: 12 and 13 (GB AY310331)**

ggggtcag
ggagggctctgtgcctccgttcagcagagctgcagctgctgccagctctcaggaggcaa
gctggactccctcactcagctgcaggagcaaggacagtgaggctcaaccccgctgagcc
atgccagccaacttcacagagggcagcttcgattccagtgggaccgggcagacgctggat
M P A N F T E G S F D S S G T G Q T L D
tcttccccagtggttgactgaaacagtgacttttactgaagtggaggaaaggaa
S S P V A C T E T V T F T E V V E G K E
tggggttccttctactactcctttaag|actgagcaattgataactctgtgggtcctcttt
W G S F Y Y S F K T E Q L I T L W V L F
gtttttaccattgttggaaactccggtgtgctttttccacatggaggagaaagaagaag
V F T I V G N S V V L F S T W R R K K K
tcaagatgaccttcttgtgactcagctggccatcacag|attctttcacaggactggtc
S R M T F F V T Q L A I T D S F T G L V
aacatcttgacagatattaattggcgattcactggagacttcacggcacctgacctgggt
N I L T D I N W R F T G D F T A P D L V
tgccgagtggtccgctatttgcag|aaaagcaagccagggtcctcattgtgatcgctgga
C R V V R Y L Q K S K P G S S L *
gcctgtcttttctgttctccattcccacccctgatcatatttgggaaggaggacactgtcca
acggtgaagtgcagtgctgggcccctgtggcctgacgactcctactggaccccatatga
ccatcgtggccttccctggtgtacttcatccctctgacaatcatcagcatcatgtatggca
ttgtgatccgaactatttggattaaaagcaaaacctacgaaacagtgatttccaactgct
cagatgggaaactgtgcagcagctataaccgaggactcatctcaaaggcaaaaatcaagg
ctatcaagtatagcatcatcatcattcttgccttcatctgctgttggagtccatacttcc
tgtttgacattttggacaatttcaacctccttccagacacccaggagcgtttctatgcct
ctgtgatcattcagaacctgccagcattgaatagtgccatcaacccctcatctactgtg
tcttcagcagctccatctctttccctgcagggagcaaagatcacaggattccagaatga
cgttccgggagagaactgagaggcatgagatgcagattctgtccaagccagaattcatct
agaccctagggcagtgccagtgctaggetgagcaccatcagctctcccagggtcctgtca
cctgcttgggcacgtgcatggaacccgagccaacttcacccccacctcgtcattacctgg
gagatgcacaagacaaatgttctaagtactgcatgcatgcttaagtattggccaacacg
aactccccagttattcatgccagccaggaaggaaacgccttcttccccaccattcccag
ccctccttcccactggccagcacctgaaccagtgaaacacaggcatttagtggtccagggt
cctggcttggagccagtgagtagac

10/539565

14/42

Figure 4F**F SEQ ID NOS: 14 and 15 (GB AY310332)**

ggggtcag
ggagggctctgtgcctccgttcagcagagctgcagctgctgccagctctcaggaggcaa
gctggactccctcactcagctgcaggagcaaggacagtgaggctcaaccccgctgagcc
atgccagccaacttcacagagggcagcttcgattccagtgggaccgggcagacgctggat
M P A N F T E G S F D S S G T G Q T L D
tcttccccagtggttgcaactgaaacagtgacttttactgaagtgggtggaaggaaaggaa
S S P V A C T E T V T F T E V V E G K E
tggggttccttctactactcctttaag|actgagcaattgataactctgtgggtcctcttt
W G S F Y Y S F K T E Q L I T L W V L F
gtttttaccattgttggaactccgttgtgctttttccacatggaggagaaagaagaag
V F T I V G N S V V L F S T W R R K K K
tcaagaatgaccttcttctgtgactcagctggccatcacag|aaaagcaagccagggtcctc
S R M T F F V T Q L A I T E K Q A R V L
attgtgatcgctggagcctgtctttctgttctccattcccaccctgatcatatttggg
I V I A W S L S F L F S I P T L I I F G
aagaggacactgtccaacggtgaagtgcagtgctgggccctgtggcctgacgactcctac
K R T L S N G E V Q C W A L W P D D S Y
tggaccccatatgacatcgctggccttccctgggtgtacttcatccctctgacaatcatc
W T P Y M T I V A F L V Y F I P L T I I
ag|catcatgtatggcattgtgatccgaactatttggattaaaagcaaacctacgaaaca
S I M Y G I V I R T I W I K S K T Y E T
gtgatttccaactgctcag|atgggaaactgtgcagcagctataaccgaggactcatctca
V I S N C S D G K L C S S Y N R G L I S
aaggcaaaaatcaaggctatcaagtatagcatcatcatcattcttg|ccttcatctgctgt
K A K I K A I K Y S I I I I L A F I C C
tggagtcataacttctgtttgacattttggacaatttcaacctccttccagacacccag
W S P Y F L F D I L D N F N L L P D T Q
gagcgtttctatgcctctgtgatcattcagaacctgccagcattgaatagtgccatcaac
E R F Y A S V I I Q N L P A L N S A I N
cccctcatctactgtgtcttcagcagctccatctcttccctcctgag|ggagcaaagatca
P L I Y C V F S S S I S F P C R E Q R S
caggattccagaatgacgttccgggagagaactgagaggcatgagatgcagattctgtcc
Q D S R M T F R E R T E R H E M Q I L S
aagccagaattcatctagaccctagggcagtgccagtgctaggtgagcaccatcagctc
K P E F I *
tcccagggtccttgtcacctgcttgggcacgtgcatggaacccgagccaacttcacccac
cctcgtcattacctgggagatgcacaagacaaatgttctaatactgcatgcactgctta
agtattggccaacacgaactccccagttattcatgccagccaggaaggaaacgccttcc
tccccaccattcccagccctccttcccactggccagcacctgaacccagtgaaacacaggc
attagtgggtccagggtcctggcttggagccagtgagtagac

10/539565

15/42

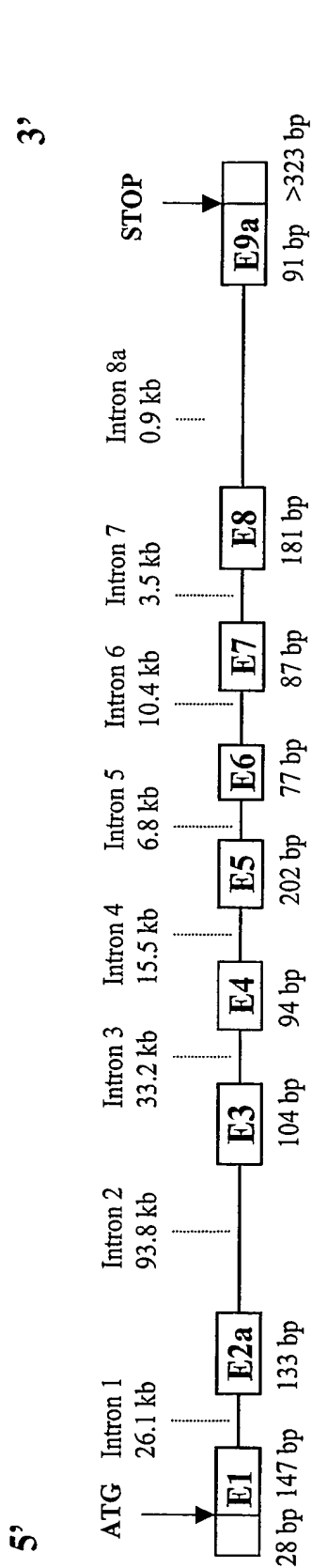


Figure 5A

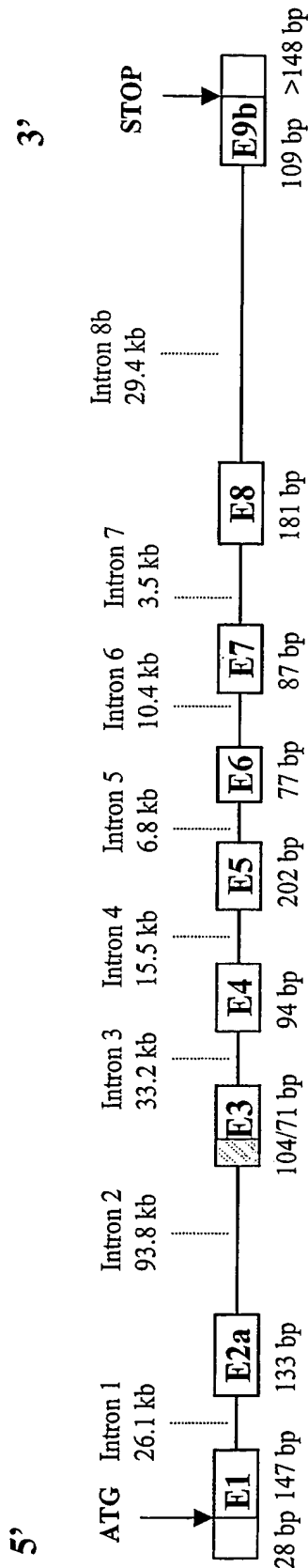


Figure 5B

10/539565

16/42

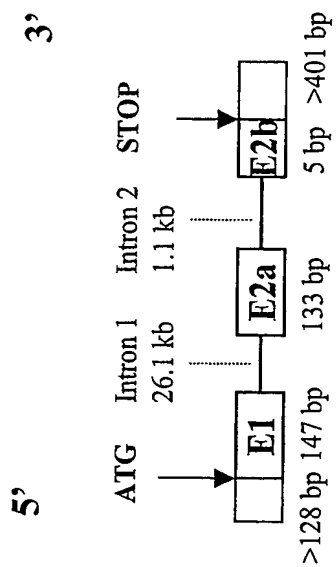


Figure 5C

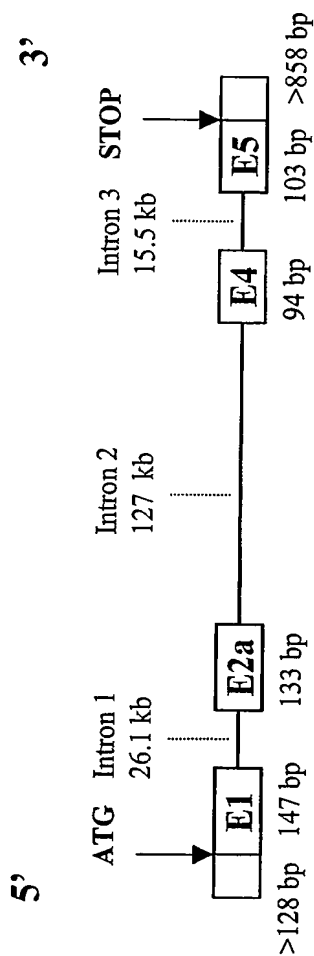


Figure 5D

10/539565

17/42

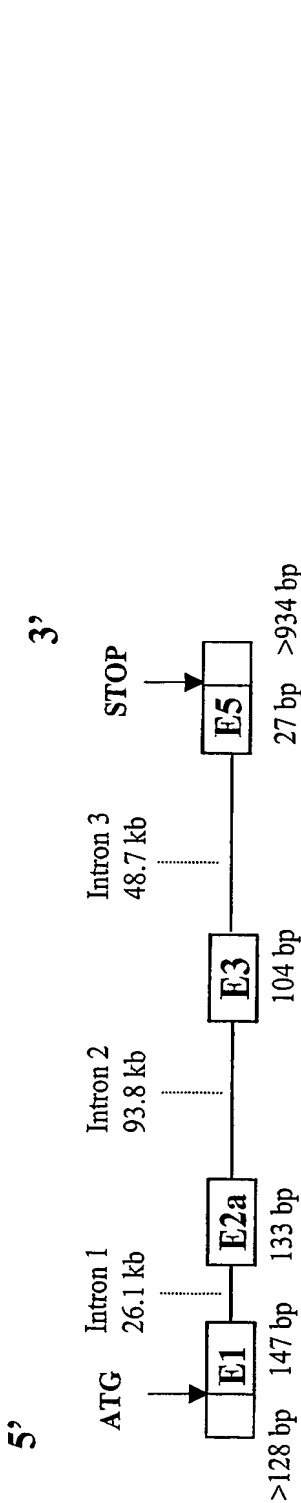


Figure 5E

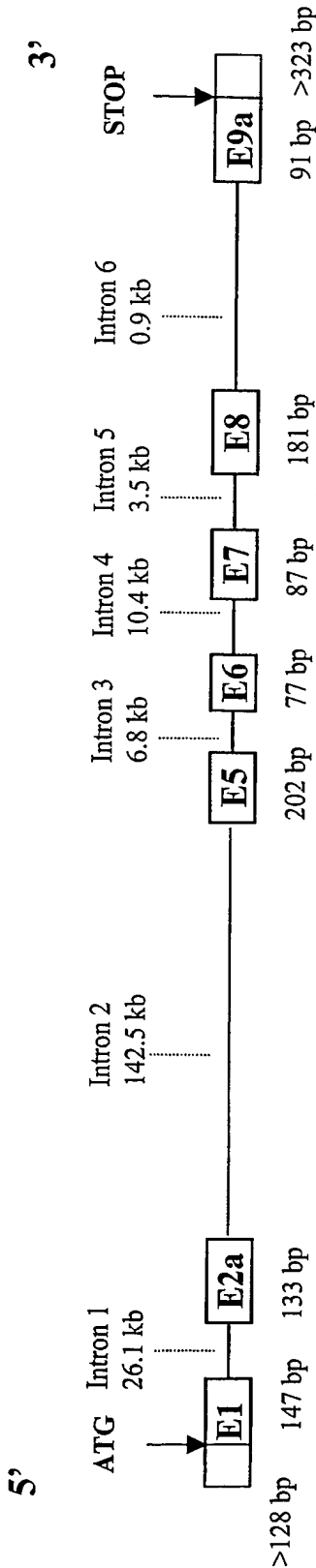


Figure 5F

10/539565

18/42

MPANFTEGSFDSSGTGQTLDSSPVACTETVTFTEVVEGKEWGSFYYSFKT

TM1 CYTOLOOP1 TM2
EQLITLWVLFVFTTIVGNSVVLFFSTWRRKKKSRMTFFVTQLAITDSFTGLV

EXOLOOP1 TM3
NILTDINWRFTGDFTAPDLVCRVVRYLQVLLYASTYVLVSLSIDRYHAI

CYTOLOOP2 TM4 EXOLOOP2
VYPMKFLQGEKQARVLIVIAWSLSFLFSIPTLIIFGKRTLSNGEVQCWAL

TM5 CYTOLOOP3
WPDDSYWTPYMTTIVAFVLVYFIPLTIISIMYGIVIRTIWIKSKTYETVISN

TM6
CSDGKLCSSYNRGLISKAKIKAIKYSIIIIILAFICCWSPYFLFDILDNFN

EXOLOOP3 TM7
LLPDTQERFYASVIIQNLPALNSAINPLIYCVFSSSISFP CREQRSQDSR

MTFRERTERHEMQILSKPEFI*

Figure 6A

19/42

10/539565

 B_{long}

MPANFTEGSFDSSGTGQTLDSSPVACTETVTFTEVVEGKEWGSFYYSFKT

TM1 CYTOLOOP1 TM2
EQLITLWVLFVFTIVGNSVVLFTWRRKKKSRMTFFVTQLAITDSFTGLV

EXOLOOP1 TM3
NILTDINWRFTGDFTAPDLVCRVRYLQVVLLYASTYVLVSLSIDRYHAI

CYTOLOOP2 TM4 EXOLOOP2
VYPMKFLQGEKQARVLIVIAWSLSFLFSIPTLIIFGKRTLSNGEVQCWAL

TM5 CYTOLOOP3
WPDDSYWTPYMTIVAFLVYFIPLTIISIMYGIVIRTIWIKSKTYETVISN

TM6
CSDGKLCSSYNRGLISKAKIKAIKYSIIIIILAFICCWSPYFLFDILDNFN

EXOLOOP3 TM7
LLPDTQERFYASVIIQNLPALNSAINPLIYCVFSSSISFPCRIVIRLRLQ

EAALMLCPQRENWKGTPGVP^{SWALPR*}

 B_{short} (33 bp deletion in exon 3)

MPANFTEGSFDSSGTGQTLDSSPVACTETVTFTEVVEGKEWGSF

YYSFKTEQLITLWVLFVFTIVGNSVVLFTWRRKKKSRMTFFVT

QLAITDINWRFTGDFTAPDLVCRVRYLQVVLLYASTYVLVSLSI

DRYHAI VYPMKFLQGEKQARVLIVIAWSLSFLFSIPTLIIFGKRTLS

NGEVQCWALWPDDSYWTPYMTIVAFLVYFIPLTIISIMYGIVIRTI

WIKSKTYETVISN CSDGKLCSSYNRGLISKAKIKAIKYSIIIIILAFIC

CWSPYFLFDILDNFN LLPDTQERFYASVIIQNLPALNSAINPLIYC

VFSSSISFPCRIVIRLRLQ EAALMLCPQRENWKGTPGVP

SWALPR*

Figure 6B

C

MPANFTEGSFDSSGTGQTLDSSPVACTETVTFTEVVEGKEWGSFYYSFKT
EQLITLWVLFVFTIVGNSVVLFSTWRRKKKSRMTFFVTQLAITV*

D

MPANFTEGSFDSSGTGQTLDSSPVACTETVTFTEVVEGKEWGSFYYSFKT
EQLITLWVLFVFTIVGNSVVLFSTWRRKKKSRMTFFVTQLAITGCAALRL
YLRPGVPQHRQIPCHRLPHEVPSRRKASQGPHCDRLEPVFSVLHSHPDHI
WEEDTVQR*

Figure 6C and 6D

E

MPANFTEGSFDSSGTGQTL DSSPVACTETVTFTEVVEGKEWGSFYYSFKTEQLITLWVLF
VFTIVGNSVVL FSTWRRKKKSRMTFFVTQLAITDSFTGLVNILTDINWRFTGDFTAPDLVC
RVVRYLQKSKPGSSL*

F

MPANFTEGSFDSSGTGQTL DSSPVACTETVTFTEVVEGKEWGSFYYSFKTEQLITLWVLF
VFTIVGNSVVL FSTWRRKKKSRMTFFVTQLAITEKQARVLIVIAWSLSFLFSIPTLIIFG
KRTLSNGEVQCWALWPDDSYWTPYMTIVAFLVYFIPLTIISIMYGIVIRTIWIKSKTYET
VISNCS DGKLCSSYNRGLISKAKIKAIKYSIIIIILAFICCWSPYFLFDILDNFNLLPDTQ
ERFYASV IIQNLPALNSAINPLIYCVFSSSISFPCREQRSQDSRMTFRERTERHEMQILS
KPEFI*

Figure 6E and 6F

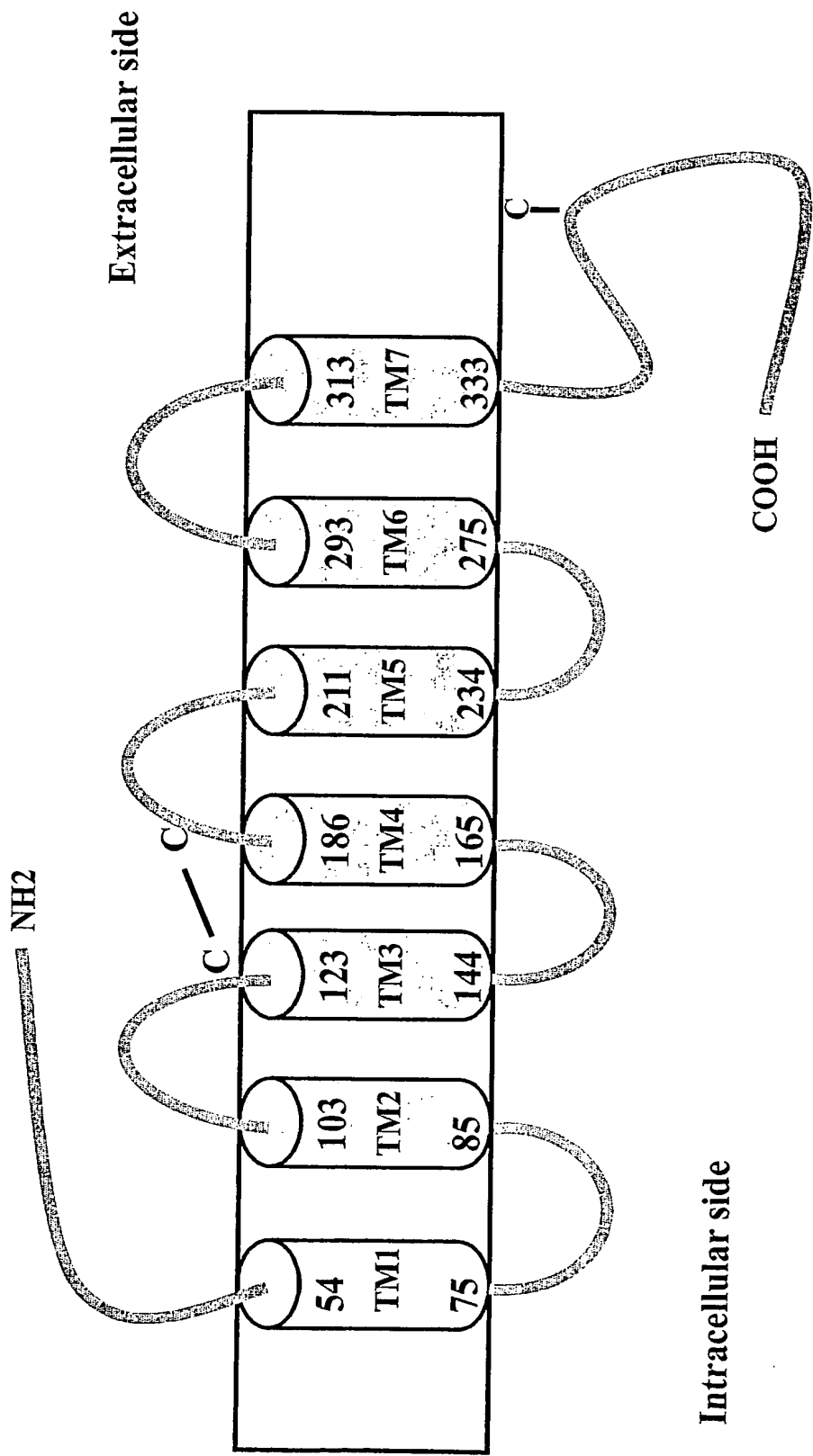


Fig. 7

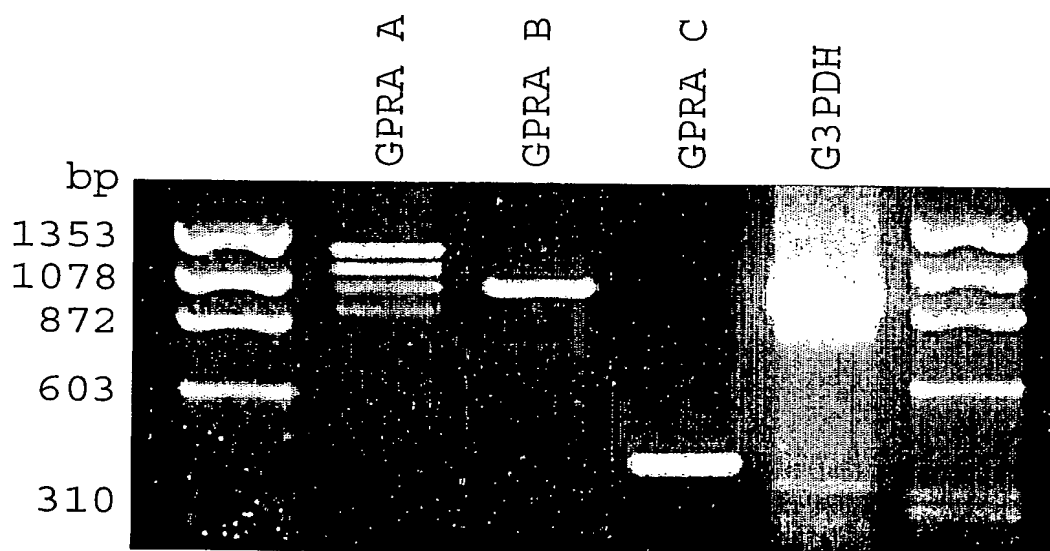


Figure 8

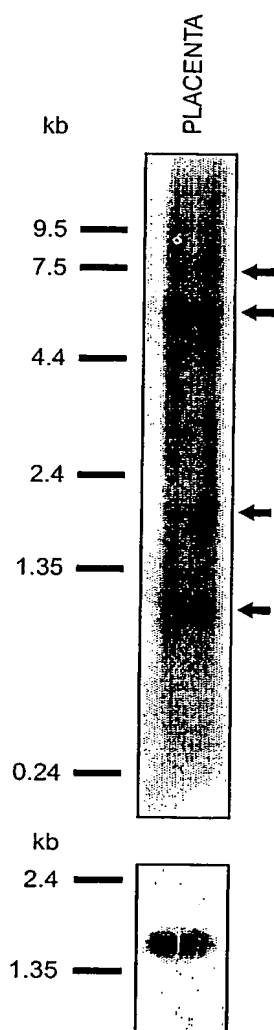


Figure 9

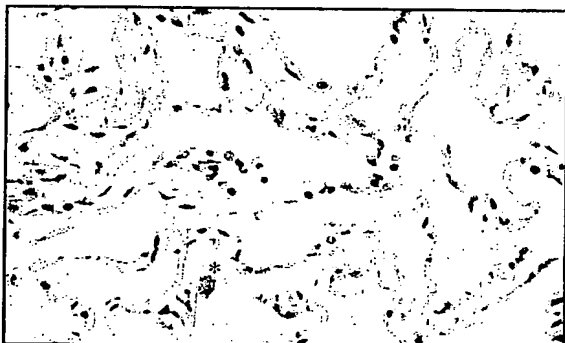
A.



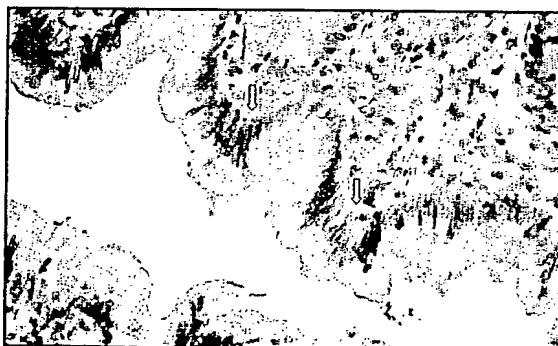
B.



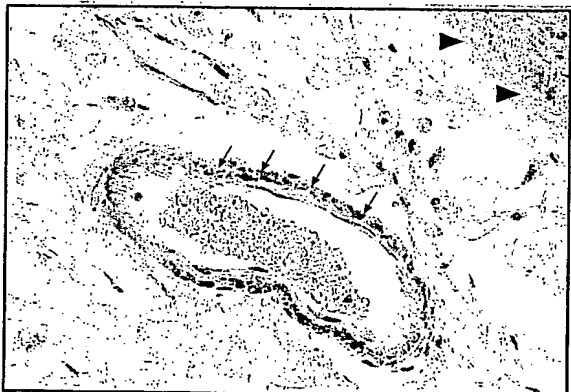
C.



D.



E.



F.

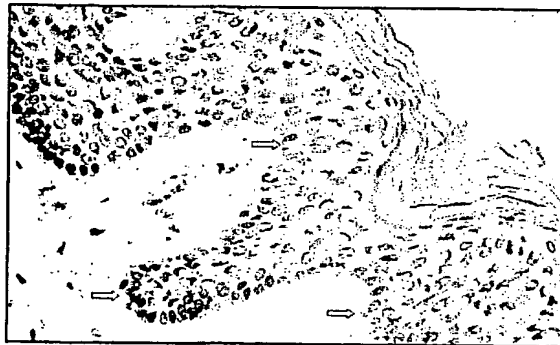


Fig. 10A, Fig. 10B, Fig. 10C, Fig. 10D, Fig. 10E, Fig. 10F

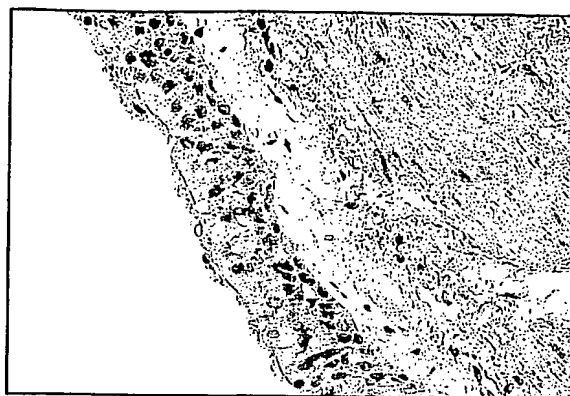
10/539565

26/42

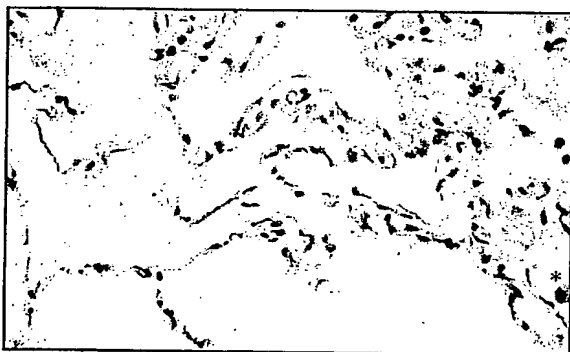
A.



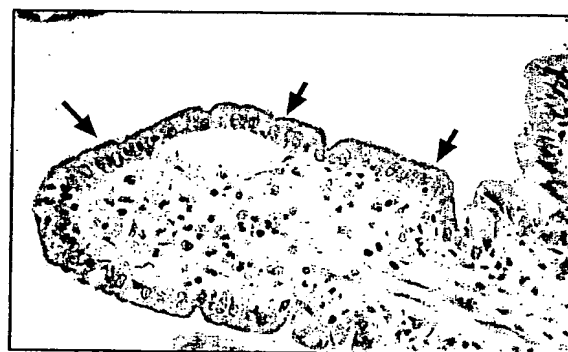
B.



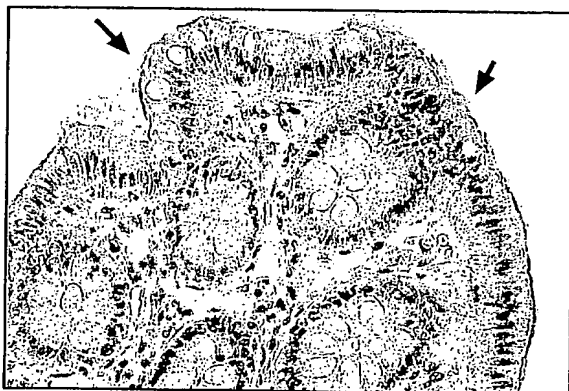
C.



D.



E.



F.

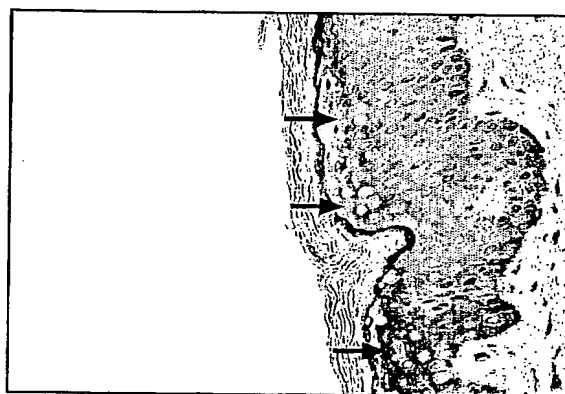


Fig. 11A, Fig. 11B, Fig. 11C, Fig. 11D, Fig. 11E, Fig. 11F

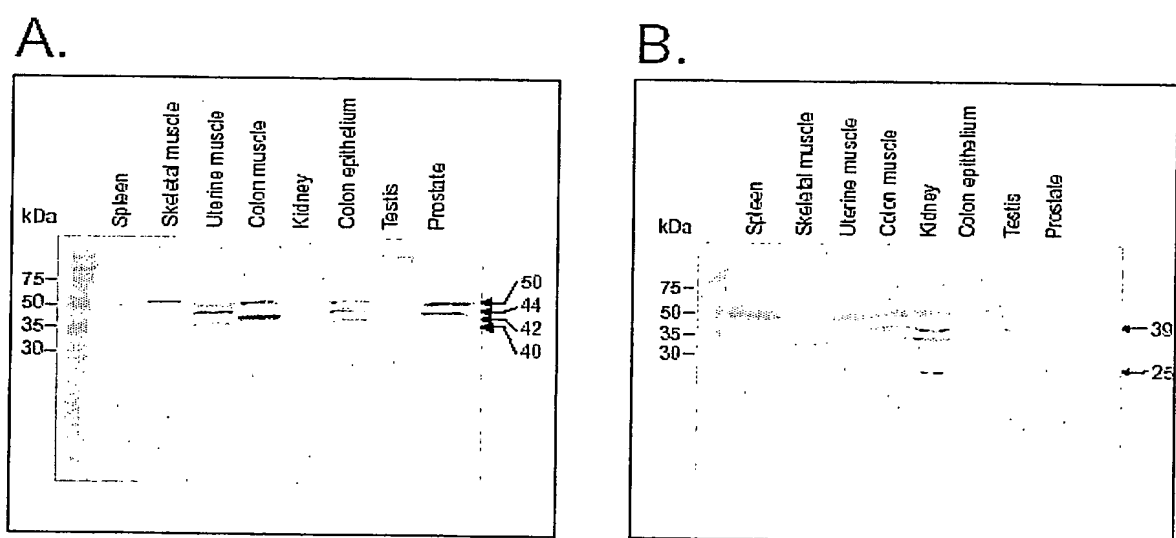


Fig. 12A and 12B

10/539565

28/42

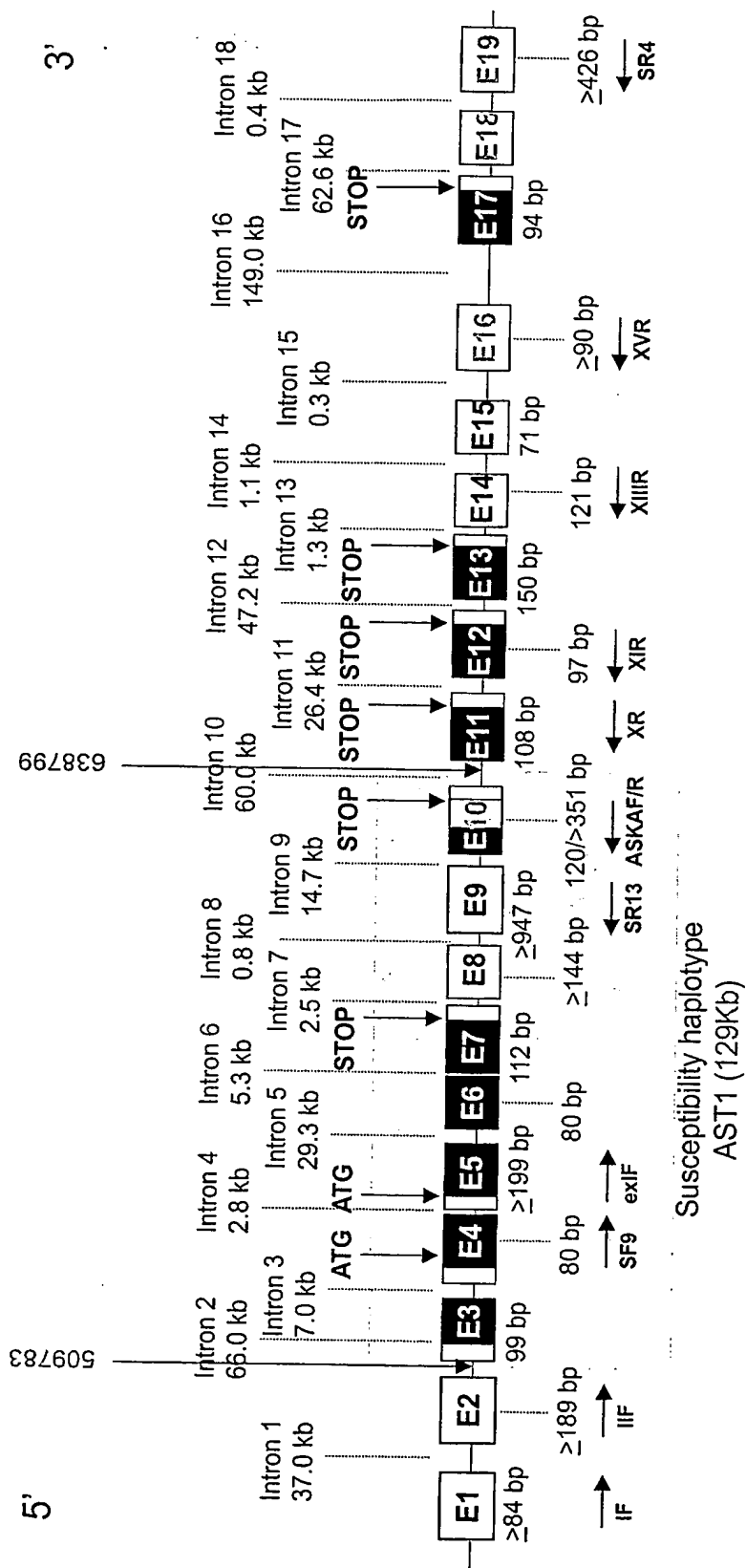


Fig. 13

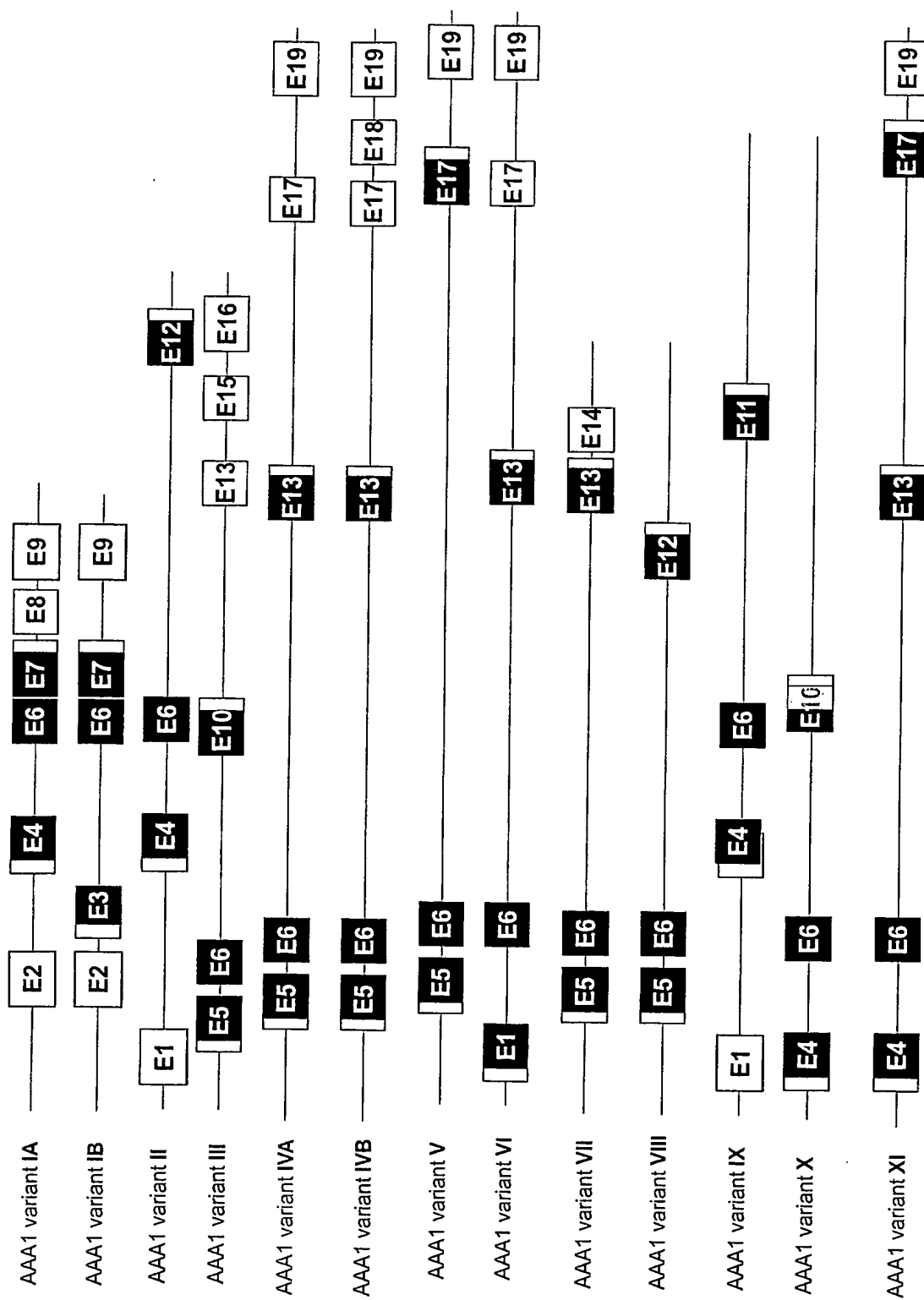


Fig. 14

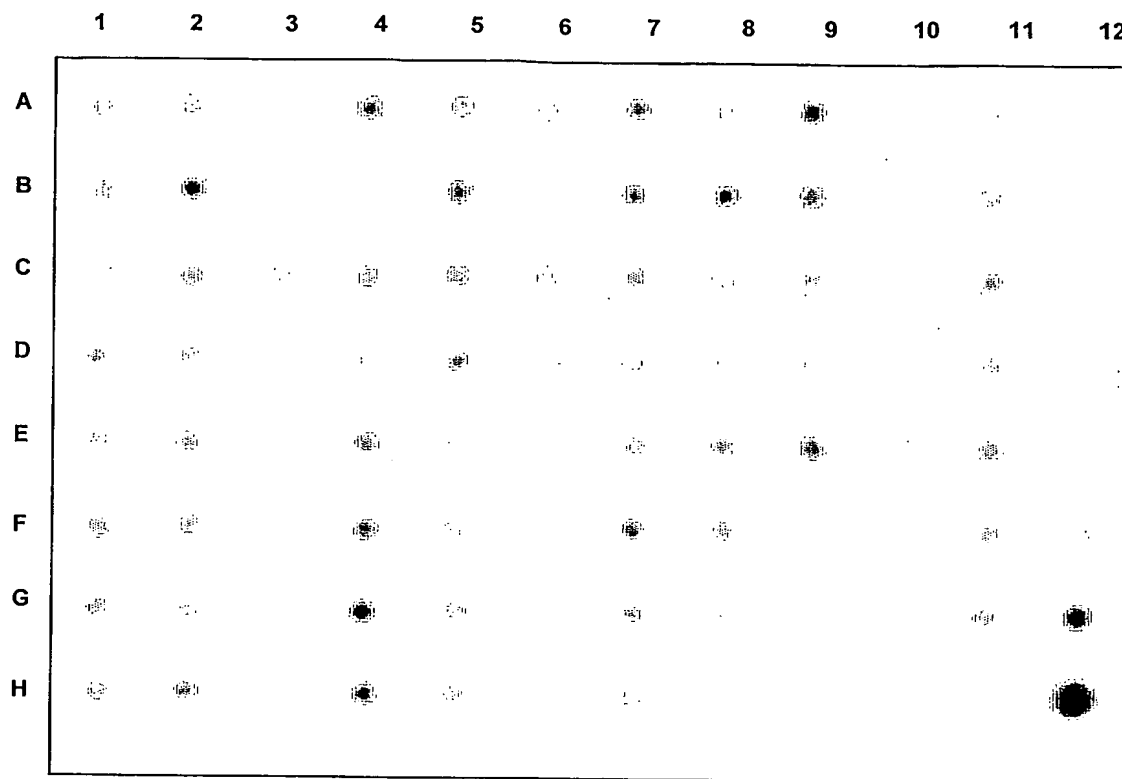
I	MQCEAGAGAYVRRNAGRRQRFSSHCHCNLHAAHQAFLVRRKQELQSVRWYFEAGLWVKDT
II	MQCEAGAGAYVRRNAGRRQRFSSHCHCNLHAAHQAFLVRRKQVNDIHCSKQHVLKRFVFSPPFNGLGTFLKN
III	MKKLKHRRPAPAYVRRNAGRRQRFSSHCHCNLHAAHQAFLVRRKQENKD
IV	MKKLKHRRPAPAYVRRNAGRRQRFSSHCHCNLHAAHQAFLVRRKQDQRLPPLSCQVGSPPGCCSARKRSHVQEH
V	MKKLKHRRPAPAYVRRNAGRRQRFSSHCHCNLHAAHQAFLVRRKQDQRLPPLSCQVGSPPGCCSARKRSHVQEH
VI	MPLDLMLERLKTLGLGDYWKAYVRRNAGRRQRFSSHCHCNLHAAHQAFLVRRKQDQRLPPLSCQVGSPPGCCSARKRSHVQEH
VII	MKKLKHRRPAPAYVRRNAGRRQRFSSHCHCNLHAAHQAFLVRRKQDQRLPPLSCQVGSPPGCCSARKRSHVQEH
VIII	MKKLKHRRPAPAYVRRNAGRRQRFSSHCHCNLHAAHQAFLVRRKQDQRLPPLSCQVGSPPGCCSARKRSHVQEH
IX	MKKLKHRRPAPAYVRRNAGRRQRFSSHCHCNLHAAHQAFLVRRKQDQRLPPLSCQVGSPPGCCSARKRSHVQEH
X	MQCEAGAGAYVRRNAGRRQRFSSHCHCNLHAAHQAFLVRRKQV
XI	MQCEAGAGAYVRRNAGRRQRFSSHCHCNLHAAHQAFLVRRKQENKD
	MQCEAGAGAYVRRNAGRRQRFSSHCHCNLHAAHQAFLVRRKQDQRLPPLSCQVGSPPGCCSARKRSHVQEH

*) shared protein coding sequence, different 3'-untranslated regions

Figure 15

10/539565

31/42



	1	2	3	4	5	6	7	8	9	10	11	12
A	whole brain	cerebellum, left		heart	esophagus	colon, transverse	kidney	lung	liver	leukemia, HL-60	fetal brain	yeast total RNA
B	cerebral cortex	cerebellum, right	accumbens nucleus	nota	stomach	colon, descending	skeletal muscle	placenta	pancreas	HeLa S3	fetal heart	yeast tRNA
C	frontal lobe	corpus callosum	thalamus	atrium, left	duodenum	rectum	spleen	bladder	adrenal gland	leukemia, K-562	fetal kidney	<i>E. coli</i> rRNA
D	parietal lobe	amygdala		atrium, right	jejunum		thyroid	uterus	thyroid gland	leukemia, MOLT-4	fetal liver	<i>E. coli</i> DNA
E	occipital lobe	caudate nucleus	spinal cord	ventricle, left	ileum		peripheral blood leukocyte	prostate	salivary gland	Burkitt's lymphoma, Raji	fetal spleen	Poly (A)
F	temporal lobe	hippocampus		ventricle, right	ileocecum		lymph node	testis		Burkitt's lymphoma, Daudi	fetal thymus	human Cyt. 1 DNA
G	p. g.* of cerebral cortex	medulla oblongata		inter-ventricular septum	appendix		bone marrow	ovary		colorectal adenocarcinoma, SW620	fetal lung	human DNA 100 ng
H	pons	putamen		apex of the heart	colon, ascending		trachea			lung carcinoma, A549		human DNA 500 ng

* para central gyrus

Figure 16

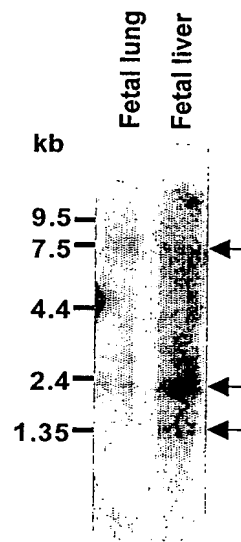


Figure 17

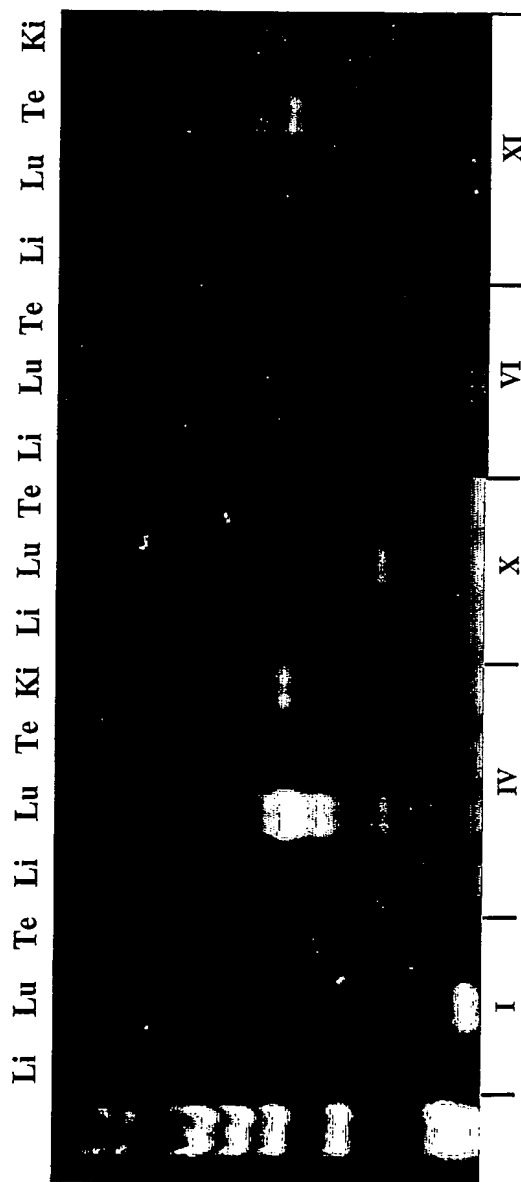


Figure 18

101539565

34/42

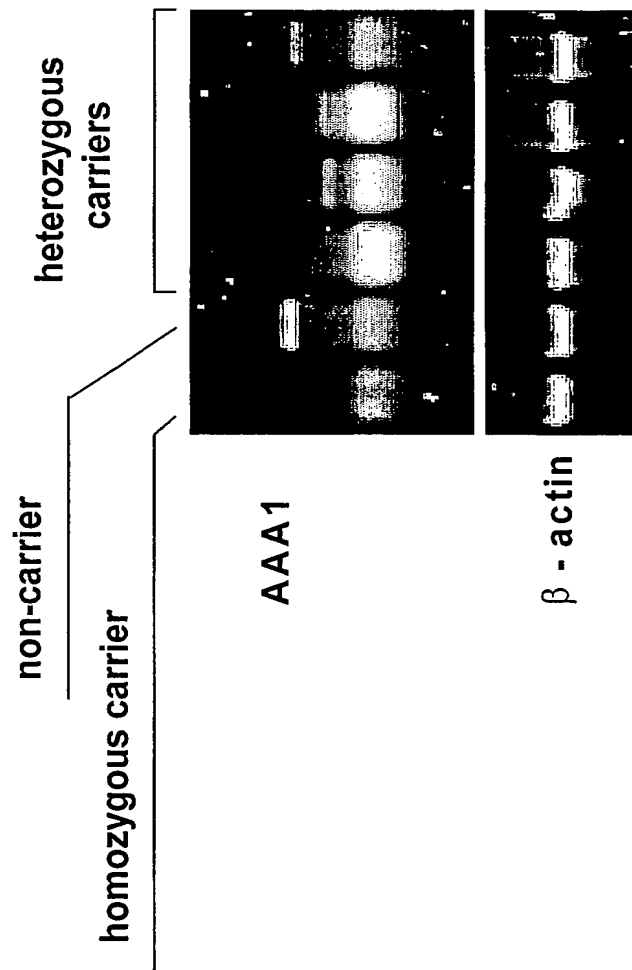


Figure 19

Figure 20

I exons 2, 4, 6, 7, 8, 9

GB AY312364

SEQ ID NOS: 16 and 17

gacacagagaagaccactccccacctccccgagtgcaaggtgtgaagggacagatcttttaac
catgcctgcccccttatacttgctgttcatagaattgcaactgaaagtgaccatgaggat
ccactggatggagttacttctttcttaagtgaggaggctaagatctggagtgacttctcc
ccagatTTTTGTatacctgactctgtttcagcatccgcttcccaaagaatgcagtgtaa
M Q C E
gcaggagcttatgtgagaagaaacgcagggagacagttcagtcactgcaatcttcatgcc
A G A Y V R R N A G R Q F S H C N L H A
catcagtttcttgtgagaagaaaacaagagctccaatctgttagatgggtattttgaagca
H Q F L V R R K Q E L Q S V R W Y F E A
ggcttttgggtaaaggacacctagacccagtgaaaggtcatgggtgattattattggacaat
G L W V K D T
gggacatcactctgctatttgaacaaataagactttttcctgacatgcatctggaggcag
gtcaaagctccaggccaactccaagtttctgatggggctctctagccaatggaaggcttct
tctccttcaattgcctgactcttcaggactcttaataactgcaaagtgagaaaatgagac
aggttgcactgagggctgttagccagacagagtctcgaactggaagtccatctagatggt
ttgcataagagaatggaaacaatctgtctgtgatttagggacatactctggcagcaatat
gggaatacagtttcaatcctcattaacaaaacaggtatgaaatacatatttatttagtaa
gggtgccagctgtatgaaaaatccatttcttatttcccataatgtttctgaaatgtcttag
cagtgcatagagacagcatgtcatcattttctagggactgtgtgttattgcatttttctc
aggggaagatcttttctaggtcacctgtccttcgctaaagctctgaccaatctagcttgc
taacctgtgactccattttcctaagtcctgagagagaaaaacgcttgcagcaaattatg
ccaggcatccttgtgtctaaatgaaaaaaggaaaaagcctccttccctctgttgag
aagtgcacgggtccacatatgcatgcacagcatatactgtgaggggtatttgcagtccttgc
ggttgcttggataactggccaggttgcgtgttctatttttccacattctattaatcctcct
acaggcagttattaggtattgagtgtcacacacccctggcatagtcaccacatgccatt
agctccagataaaacttccagaaaaaagtcacatccccacttctctcagctgcctgccaac
gctggacaccttctaccaagccagcaggacagagaaaagcctgggctttaagatcaaac
aaacacagcttcaaattaggactctgtcacttctgtgtactgggcactttgctgagtat
gtgggttctcatctgtaaaacagagaaagatgattatctcccaatctttctatgttatat
gtttgaattaaataaggtactctccatgaa

Figure 20 (continued)

III exons 5, 6, 10a, 13, 15, 16

GB AY 312367 SEQ ID NOS: 22 and 23

tctaggactcagaaatatagatggttagtaagagcaaacagacataacagataacacatac
aaagtgcctaccacatgctaaccactgctgcaggcactttctatagaagaactaatttaa
tcatcaccataaccctatggggtagatgatatttttacaacctccattttacagatgaag
M K
aaactgaagcatagacctgcttatgtgagaagaaacgcagggagacagttcagtcactgc
K L K H R P A Y V R R N A G R Q F S H C
aatcttcatgcccacagtttcttgtgagaagaaaacaagaaaacaaggactgaaatcca
N L H A H Q F L V R R K Q E N K D
cacaggaaggtggcagtgaaactccacagacggacctggacgcctcaacactcctggcctt
acctcccttgctgaacgtctcaagtttctctgcgttcaggactggcaacgcctgcttctt
cctctgagctgtcaagtaggaagtcggggtgctctgctagaaagagaagtcattgtgcag
gagcactgaggcatcccaggtgtgacactcttccacctagagcattccgtctctcatcct
ctgccatgtgacgctgggcttctttaacaaattaatcccaagtgaagacattttatttct
tctgtacctaatgacctgagcaatccttctctgctgaacctggtagtgcattcttagaa
gtgaagacacaattaacacatgggtcatttcttcattatatcgttgttact

IV exons 5, 6, 13, 17, 19

GB AY312368 SEQ ID NOS: 24 and 25

tctaggactcagaaatatagatggttagtaagagcaaacagacataacagataacacatac
aaagtgcctaccacatgctaaccactgctgcaggcactttctatagaagaactaatttaa
tcatcaccataaccctatggggtagatgatatttttacaacctccattttacagatgaag
M K
aaactgaagcatagacctgcttatgtgagaagaaacgcagggagacagttcagtcactgc
K L K H R P A Y V R R N A G R Q F S H C
aatcttcatgcccacagtttcttgtgagaagaaaacaagactggcaacgcctgcttctt
N L H A H Q F L V R R K Q D W Q R L L P
cctctgagctgtcaagtaggaagtcggggtgctctgctagaaagagaagtcattgtgcag
P L S C Q V G S P G C S A R K R S H V Q
gagcactgaggcatcccaggtgtgacactcttccacctagagcattccgtctctcatcct
E H
ctgccatgtagcaaactgctatgcatccttcagctgcaagggattgaatgctatcaacaa
ccatacaagtggaagcagatgcttccctagctgagcctcaggctttttgatggaattg
ctacaacttgggtgcatgcctgctcctaaaagaaataactcaggaattgtctcataaagtcc
tcacctactggcaaaaacaagatgttctactcccaggttgactttttcaagccccaagat
gttgagtcagccatttctccaaggatctcgatttcttttaattggaaaataacattaaaca
ccaaatataagcctcgctgtcccacatgcgtattggggacaagatgaaacctgcttccag
gctacttttggcagcagaactgaaaaaggcttttttccagatatatgatttctcatcgac
agggttgacagccctctttattgttcgtgtaaatgacacccttggatctgaacaatata
caccaggacaattgtgtgcaacagttctacaaactgatatttctaatta

Figure 20 (continued)

IVB exons: 5, 6, 13, 17, 18, 19

SEQ ID NOS: 26 and 27

gtctaggactcagaaatatagatgtttagtaagagcaaacagacataaacagataaacacatac
 aaagtgcctaccacatgctaaccactgctgcaggcacttttctatagaagaactaatttaa
 tcatcaccataaaccctatggggtagatgatatttttacaacctccattttacagatgaag
 M K
 aaactgaagcatagacctgcttatgtgagaagaaacgcagggagacagttcagtcactgc
 K L K H R P A Y V R R N A G R Q F S H C
 aatcttcatgcccacagtttcttgtgagaagaaaacaagactggcaacgcctgcttcct
 N L H A H Q F L V R R K Q D W Q R L L P
 cctctgagctgtcaagtaggaagtccgggctgctctgctagaaagagaagtcagtgtag
 P L S C Q V G S P G C S A R K R S H V Q
 gagcactgagggcatcccaggtgtgacactcttccacctagagcattccgtctctcactct
 E H
 ctgccatgtagcaaaactgctatgcacccctcagctgcaagggattgaatgctatcaacaa
 ccatacaagtggagaagcagatgcttccctagctgagcctcagctctgttttcctcagtc
 ctaggggcagattctaatttgggtacagaaaaaaaagtagctcctgccaattcccactctg
 gaatgactgaagaaaagaaaatgcatgtgattattttaaggctttttgatggaattgct
 acaacttgggtgcatgcctgctcctaaaagaaatactcaggaattgtctcataaagtcctc
 acctactggcaaaaaacaagatgttctactcccaggttgactttttcaagccccaagatgt
 tgagttagccatttctccaaggatctcgatttcccttttaattggaaaataacattaaacacc
 aaatataagcctcgctgtcccacatgcgtattggggacaagatgaaacctgcttccaggc
 tactttggcagcagaactgaaaaaggcttttttccagatatatgatttctcatcgacag
 ggttgacagccctctttattgttcgtgtaaatgacacccttggatctgaacaatacaca
 ccaggacaattgtgtgcaacagttctacaaactgatatttctaatta

V exons 5, 6, 17, 19

GB AY 312369 SEQ ID NOS: 28 and 29

tctaggactcagaaatatagatgtttagtaagagcaaacagacataaacagataaacacatac
 aaagtgcctaccacatgctaaccactgctgcaggcacttttctatagaagaactaatttaa
 tcatcaccataaaccctatggggtagatgatatttttacaacctccattttacagatgaag
 M K
 aaactgaagcatagacctgcttatgtgagaagaaacgcagggagacagttcagtcactgc
 K L K H R P A Y V R R N A G R Q F S H C
 aatcttcatgcccacagtttcttgtgagaagaaaacaagcaaaactgctatgcacccct
 N L H A H Q F L V R R K Q S K L L C I L
 cagctgcaagggattgaatgctatcaacaaccatacaagtggagaagcagatgcttccct
 Q L Q G I E C Y Q Q P Y K W R S R C F P
 agctgagcctcaggcctttttgatggaattgctacaacttgggtgcatgcctgctcctaaaa
 S
 gaaatactcaggaattgtctcataaagtcctcacctactggcaaaaaacaagatgttctac
 tcccagggttgactttttcaagccccaagatgttgagttagccatttccaaggatctcga
 tttccttttaattggaaaataacattaaacaccaaataaagcctcgctgtcccacatgcg
 tattggggacaagatgaaacctgcttccaggctactttggcagcagaactgaaaaaggct
 ttttttccagatatatgatttctcatcgacagggttgacagccctctttattgttcgtg
 taaatgacacccttggatctgaacaatacacaccaggacaattgtgtgcaacagttctac
 aaactgatatttctaatta

Figure 20 (continued)

IB: exons 2, 3, 6, 7, 9

GB AY312365 SEQ ID NOS: 18 and 19

gacacagagaagaccactcccacctccccgagtgcagggtgtgaagggacagatctttta
accatgcctgcccccttatacttgctgttcatagaattgcaactgaaagtgaccatgagg
atccactggatggagttacttctttcttaagtgaggaggctaagatctgagttcttcaca
tctctctgtagataaaaatttccgggtctggtttcacattcctctgtcagaagaactttctt
taatgtttcttaaagtacaggtctgctgcttatgtgagaagaaacgcagggagacagttc
C F L K Y R S A A Y V R R N A G R Q F
agtcactgcaatcttcatgcccacagtttcttgtagaagaaaacaagagctccaatct
S H C N L H A H Q F L V R R K Q E L Q S
gttagatgggtattttgaagcaggtctttgggtaaaggacacctagaccagtgagggtca
V R W Y F E A G L W V K D T
tggtgattattattggacaatgggacatcactctgctattaagtgagaaaatgagacagg
ttgcactgagggctgttagccagacagagttctcgaactggaagtccatctagatgttttg
cataagagaatggaaacaatctgtctgtgatttagggacatactctggcagcaatatggg
aatacagtttcaatcctcattaacaaaacaggtatgaaatacatatttattagtaagggt
gccagctgtatgaaaaatccatttcttatttcccataatgtttctgaaatgtcttagcag
tgcataagacagcatgtcatcatttcttagggactgtgtgttattgcatttttcttagg
gaagatcttttctaggtcacctgctccttcgctaaagctctgaccaatctagcttgctaa
cctgtgactccatttttcttaagtcctgagagagaaaaacgctttgcagcaaattatgcca
ggcatccttgtgtctaaatgaaaaaaggaaaaagcctccttccctctgttgagaag
tgcacggtccacatatgcatgcacagcatatactgtgaggggtatgtgcagtccttgggt
tgctttgataactggccaggttgctgttctattttccacattctattaatcctcctaca
ggcagttattaggtattgagtgtcacacacccctggcatagtcaccacatgccattagc
tccagataaaacttccagaaaaaagtcacatccccacttctctcagctgctgccaacgt
ggacaccttctaccaagccagcaggacagagaaaagcctgggctttaagatcaaacaaa
cacagcttcaaattaggactctgtcacttccctgtgtactgggcactttgtgtgagtatgtg
gtttctcatctgtaaaacagagaaagatgattatctcccaatctttctatgttatatgtt
tgaattaaataaggtactctccatgaa

II exons 1, 4, 6, 12

GB AY312366 SEQ ID NOS: 20 and 21

gctgatgggtggaaggagaatgagttctctgatgcctttggacttgatgctggaaagacttaa
gactttgggggactactggaaaggagtgacttctccccagatttttgtatacctgactct
gtttcagcatccgcttcccaaagaatgcagtggtgaagcaggagcttatgtgagaagaac
M Q C E A G A Y V R R N
gcagggagacagttcagtcactgcaatcttcatgcccacagtttcttgtagaagaaaa
A G R Q F S H C N L H A H Q F L V R R K
caagtggatatacactgttccaagcagcatgtgttgaaaagattttgtcttttcccat
Q V D I H C S K Q H V L K R F V F S P F
aatgggtcttggtacctttctcaaaaattgaccatatatga
N G L G T F L K N

Figure 20 (continued)

VI exons 1, 6, 13, 17, 19

GB AY 312370 SEQ ID NOS: 30 and 31

gctgatgggtggaaggagaatgagtcctctgatgcctttggacttgatgctggaaagacttaag
M P L D L M L E R L K
actttgggggactactggaaagccttatgtgagaagaaacgcagggagacagttcagtcac
T L G D Y W K A Y V R R N A G R Q F S H
tgcaatcttcatgcccacagtttcttgtgagaagaaaacaagactggcaacgcctgctt
C N L H A H Q F L V R R K Q D W Q R L L
cctcctctgagctgtcaagtaggaagtccgggctgctctgctagaaagagaagtcagtg
P P L S C Q V G S P G C S A R K R S H V
caggagcactgaggcatcccaggtgtgacactcttccacctagagcattccgtctctcat
Q E H
cctctgccatgtagcaaaactgctatgcatccttcagctgcaagggattgaatgctatcaa
caaccatacaagtggagaagcagatgcttccctagctgagcctcaggctttttgatggaa
ttgctacaacttgggtgcatgcctgctcctaaaagaaataactcaggaattgtctcataaag
tctcacctactggcaaaaacaagatgttctactcccaggttgactttttcaagcccaaa
gatgttgagtcagccattctccaaggatctcgatttcccttttaattgaaaaataacattaa
acaccaaataataagcctcgctgtcccacatgcgtattggggacaagatgaaacctgcttc
caggctacttttggcagcagaactgaaaaaggcttttttccagatatatgatttctcatc
gacagggttgacagccctctttattgttctgtgtaaatgacacccttggatctgaacaat
acacaccaggacaattgtgtgcaacagttctacaaactgatattttctaatta

VII exons 5, 6, 13, 14

GB AY 312371 SEQ ID NOS: 32 and 33

tctaggactcagaaatatagatgttagtaagagcaaacagacataacagataacacatac
aaagtgcctaccacatgctaaccactgctgcaggcactttctatagaagaactaatttaa
tcatcaccataaccctatggggtagatgatatttttacaacctccattttacagatgaag
M K
aaactgaagcatagacctgcttatgtgagaagaaacgcagggagacagttcagtcactgc
K L K H R P A Y V R R N A G R Q F S H C
aatcttcatgcccacagtttcttgtgagaagaaaacaagactggcaacgcctgcttct
N L H A H Q F L V R R K Q D W Q R L L P
cctctgagctgtcaagtaggaagtccgggctgctctgctagaaagagaagtcagtgtag
P L S C Q V G S P G C S A R K R S H V Q
gagcactgaggcatcccaggtgtgacactcttccacctagagcattccgtctctcatcct
E H
ctgccatgtgccatgttttgaaccactagattagaggggtcaagcaattttcttggaaattt
actctgaattctacgtagaccatttttcatgtgtatacctcctctgagtcaccctcaggta
gggacatttt

Figure 20 (continued)

VIII exons 5,6,12

GB AY 312372

SEQ ID NOS: 34 and 35

tctaggactcagaaatatagatggttagtaagagcaaacagacataacagataaacacatac
aaagtgcctaccacatgctaaccactgctgcaggcacttttctatagaagaactaatTTAA
tcataccataaacctatggggtagatgataTTTTTACAACCTCATTttacagatgaag
M K
aaactgaagcatagacctgcttatgtgagaagaaacgcagggagacagttcagtcactgc
K L K H R P A Y V R R N A G R Q F S H C
aatcttcatgcccatacagtttcttgtgagaagaaaacaagtggatatacactgttccaag
N L H A H Q F L V R R K Q V D I H C S K
cagcatgtgtgaaaagatttgtcttttccccatttaattggtcttggtacctttctcaaa
Q H V L K R F V F S P F N G L G T F L K
aattgaccatatatga
N

IX exons 1, 4, 6, 11

GB AY 312373 SEQ ID NOS: 36 and 37

gctgatgggtggaaggagaatgagtcctctgatgcctttggacttgatgctggaagacttaa
gactttgggggactactggaaaggagtgacttctccccagatttttgtatacctgactct
gtttcagcatccgcttcccaaagaatgcagtgatgaagcaggagcttatgtgagaagaaac
M Q C E A G A Y V R R N
gcagggagacagttcagtcactgcaatcttcatgcccatacagtttcttgtgagaagaaaa
A G R Q F S H C N L H A H Q F L V R R K
caagtttaggaaaacttctacaccttctttgttgggatgttctctggactaatgactcc
Q V
aggcgagaccaccgttgatcatgaactcactttgaaacagaagctgggttggaagactg
gagctact

X exons 4, 6, 10b

GB AY 321515 SEQ ID NOS: 38 and 39

gagtgacttctccccagatttttgtatacctgactctgtttcagcatccgcttcccaaaga
atgcagtgatgaagcaggagcttatgtgagaagaaacgcagggagacagttcagtcactgc
M Q C E A G A Y V R R N A G R Q F S H C
aatcttcatgcccatacagtttcttgtgagaagaaaacaagaaaacaaggactgaaatcca
N L H A H Q F L V R R K Q E N K D
cacaggaaggtggcagtgaaactccacagacggacctggacgcctcaacactcctggcctt
acctcccttgctgaacgtctcaagtttctctgcgttcaggtaattgtataggagggttatg
agggcagagaattcctaagctcattagtaaattgctcttcagaaaagtgccttgaagcaa
agctaatttctttcccaatatgagaagatttggccctaccagaaaaaggaaatgatttg
aatgtgcgccaaaaaatatgttttctttcttttctttgttgaacactcatcgggagttac
tcttattagttccgcattttttattgccattt

Figure 20 (continued)

XI exons 4, 6, 13, 17, 19

GB AY 321516 SEQ ID NOS: 40 and 41

gagtgacttctccccagatttttgtatacctgactctgtttcagcatccgcttcccaaaga
atgcagtggtgaagcaggagcttatgtgagaagaaacgcagggagacagttcagtcactgc
M Q C E A G A Y V R R N A G R Q F S H C
aatcttcatgcccacagtttcttgtgagaagaaaacaagactggcaacgcctgcttcct
N L H A H Q F L V R R K Q D W Q R L L P
cctctgagctgtcaagtaggaagtccgggctgctctgctagaaagagaagtcattgtgcag
P L S C Q V G S P G C S A R K R S H V Q
gagcactgagggcatcccagggtgtgacactcttccacctagagcattccgtctctcatcct
E H
ctgccatgtagcaaaactgctatgcaccccttcagctgcaagggattgaatgctatcaacaa
ccatacaagtggaagcagatgcttccctagctgagcctcaggctttttgatggaattg
ctacaacttggtgcatgcctgctcctaaaaagaaatactcaggaattgtctcataaagtcc
tcacctactggcaaaaaacaagatgttctactcccagggttgactttttcaagccccaagat
ggtgagtcagccattctccaaggatctcgatttccttttaattggaaaataacattaaaca
ccaaatataagcctcgctgtcccacatgcgtattggggacaagatgaaacctgcttccag
gctactttggcagcagaactgaaaaaggctttttttccagatatatgatttctcatcgac
agggttgacacagccctctttattgttcgtgtaaatgacacccttggaatctgaacaatata
caccaggacaattgtgtgcaacagttctacaaactgatattttctaatta

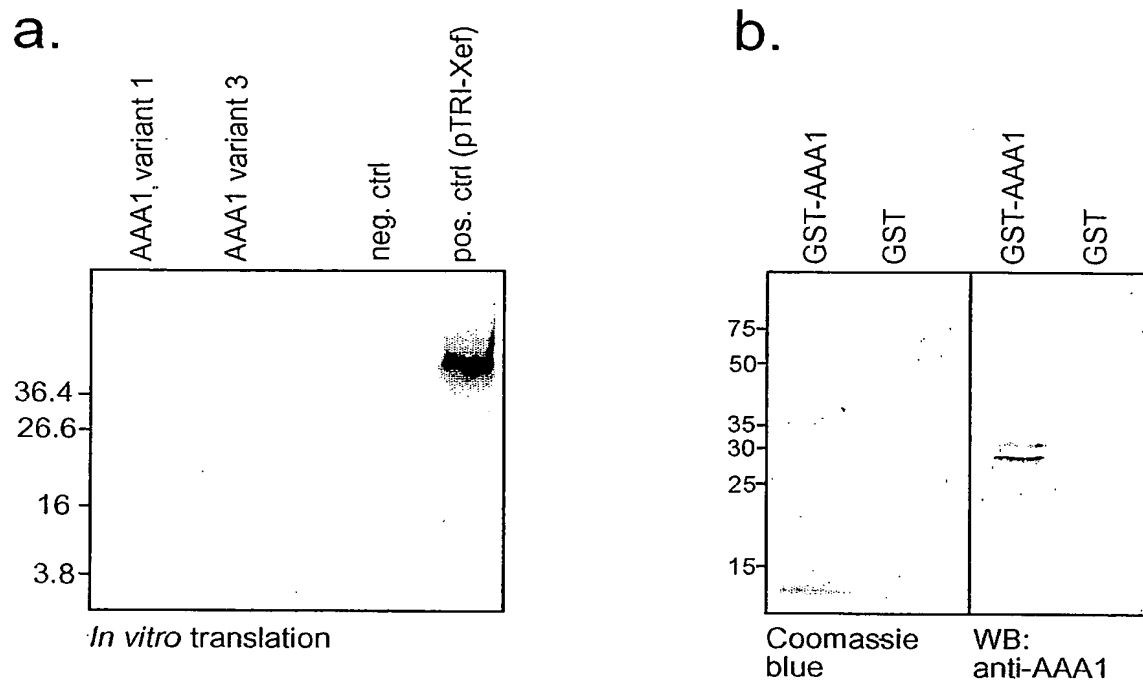


Fig. 21A and 21B